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Post-processing: Minimum Match 0%
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Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Database :
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Maximum DB seq length: 2000000000
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11689.493 Million cell updates/sec
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1: gb_ba:
2: gb_htg
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Gapop 10.0 , Gapext 1.0
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3625
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gb_htg:*
gb_in:*
em_htgo_hum:*
em_htgo_mus:*
em_htgo_other:*
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Searched:

Sequence:

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1	NO. 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result
-	Score 3162.8 3294.8 2294.8 2294.6 22004.6 2004.6 2003.2 21632.2 2023.2 2023.2 2023.2 2023.6 21632.2 11632.3 6 1188.6 1118.6 11174.6 6 11174.6 11175.8 11155.8 11155.8 11155.8 11155.8 11155.8 11155.8 11169.4 11161.1 11155.8 11169.4 11169.4 1169.4 1169.8 1179.6	
	Match 63.4 63.4 58.1 57.8 57.8 57.8 57.8 56.0 32.8 32.8 32.3 32.3 32.3 32.3 32.3 32.1 32.3 32.3	Query
	Length 3953 2457 2457 2457 2457 2457 2457 2457 2457	
	DB 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	
ALIGNMENTS	HSCLCN3 AF029346 AF029346 AF029348 AF029348 AF029348 RATCLC3 AMMCLCNS CPUB3464 AF132214 AF132214 AF132215 AF182215 RNCHCHANP HSCLCN5GN AR056560 AF195533 AK092049 AF074925 AF134117 AB019432 AF134117 AB019432 AF134117 AF14117 AF14	
	Description X78520 H. sapiens AF029346 Homo sapi AF172729 Homo sapi AF172729 Homo sapi AF172729 Homo sapi AF029348 Gryctolage AF029348 Gryctolage AF029348 Gryctolage D17521 Rat mRNA fo X78874 M.musculus U83464 Cavia por AF13277 Rattus nor AF029347 Wis muscu V9941 Xenopus lae AF182215 Tilapia m Z36644 R. norvegicu X91906 H. sapiens v AK056560 Homo sapi AF195523 Oryctolage AF02049 Homo sapi AF195523 Oryctolage AF032049 Homo sapi AF197492 Homo sapi AF177492 Homo sapi AF177492 Homo sapi AF177492 Homo sapi AF177497 Homo sapi AF177497 Homo sapi AF177497 Homo sapi AF176492 Homo sapi AF182216 Tilapia m BC005553 Mus muscu AY12943 Drosophil AF13215 Cavia por AF347684 Mus muscu AF133215 Cavia por AF347688 Mus muscu AF133215 Cavia por AF347684 Mus muscu AF1374684 Mus muscu AF137216 Cavia por AF347684 Mus muscu AF137216 Cavia por AF347684 Mus muscu AF137216 Cavia por AF347684 Mus muscu AF137219 Homo sapi AC069491 Homo sapi AC069293 Human DNA X81836 H. saplens m AC014422 Drosophil	

TITLE	AUTHORS	REFERENCE			ORGANISM	SOURCE		KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	RESULT 1 HSCLCN3	
Characterization of a human and murine gene (CLCN3) sharing	Borsani, G., Rugarli, E.I., Taglialatela, M., Wong, C. and Ballabio, A.	1 (bases 1 to 3953)	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens	Homo sapiens.	CLCL3 gene.	chloride channel; chloride channel 3; chloride channel protein;	X78520.1 GI:854101	X78520		HSCLCN3 3953 bp mRNA linear PRI 21-NOV-1995		

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REFERENCE
AUTHORS
TITLE
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ORIGIN
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Query Match
Best Local Similarity
Matches 3252; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        similarities to voltage-gated chloride channels and to a yeast integral membrane protein Genomics 27 (1), 131-141 (1995) 95394449
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Borsani,G.
Direct Submission
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                                                                                                                                     KKDILRHMAQTANQDPASIMFN"
766 c 940 g 11:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FSLEEVSYYFPLKTLWRSFFAALVAAFVLRSINPFGNSRLVLFYVEYHTPWYLFELFP
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NTSELIKELFTDCGPLESSSLCDYRNDMNASKIVDDIPDRPAGIGVYSAIWQLCLALI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PSLPAESPRPLKLRSILDMSPFTVTDHTPMEIVVDIFRKLGLRQCLVTHNGRLLGIIT
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489. .2951
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489. .2951
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/db_xref="taxon:9606"
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                          87.2%;
98.0%;
Score 3162.8; Pred. No. 0; Mismatches
                                                                                                                                             1136 t
                                                         DB 9;
  47;
  Indels
                                                      Length 3953;
  21;
Gaps
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1316 1727	ATTCTTCTAGGGGTATTTGGAGGGCTTTGGGGAGCCTTTTTCATTAGGGCAAATATTGCC	1257 1668	Qу
1256 1667	CTGGTCCTTTTTATGTGGAGTATCATACACCATGGTACCTTTTGAACTGTTTCCTTTT		. Db
1196 1607	TITGCTGCTTTAGTGGCTGCATTTGTTTTGAGGTCCATCAATCCATTTGGTAACAGCCGT		Qy Db
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1076 1487	CTATCAGCTGCCTCAGCTGCAGGGGTTTCTGTAGCTTTTGGTGCACCAATTGGAGGAGTT	1017 1428	Qу Дъ
1016 1427	AATATCTTTTCCTACCTCTTTCCAAAGTATAGCACAAACGAAGCTAAAAAAAA	957 1368	Qу Db
956 1367	GCATCAGGTTTGAGTTTAGGAAAAGAAGGTCCCCTGGTACATGTTGCCTGTTGCTGCGGA	897 1308	Qy Db
896 1307	AGAGGTTACTTGGGAAAATGGACTTTAATGATTAAAACCATCACATTAGTCCTGGCTGTG	837 1248	Оу
836 1247	CATATGCCTGTGGCTCTGGAATTCCAGAGATTAAAACTATTTTAAGTGGATTCATCATC	777 1188	Qy Db
776 1187	TACATCITCTGGGCCTTGAGTTTTGCCTTTCTTGCAGTTTCCCTGGTAAAGGTATTTGCT	717 1128	Оy
716 1127	GCAGAATTAATCATAGGTCAAGCAGAGGGGTCCTGGTTCTTATATCATGAACTACATAATG	1068	Qy Db
656 1067	TGGGGATCTAATGAAACAACATTTGAA 	. 597 1008	Qy Db
596 1007	ACTGACCTAAAGGAGGGCATTTGCCTTAGTGCGTTGTGGTACAACCACGAACAGTGCTGT	537 948	Qy Db
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476 887	TCAGCATGGGAAATGACAAAAAGTTTGTATGATGCGTGGTCAGGATGGCTAGTAGTAACA	417 828	Оу
416 827	TGCGAGAAAATGTAAAGACAGAGAĀAGGCATAGACGGATCAACAGCAAAAAGAAAGAA 	357 768	Фу
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	2450	2391	\sim
	2390 2807	2331 CGAAGCATTCTTGACATGAGCCCTTTTACAGTGACAGACCACACCCCAATGGAGATT	გ გ
	2330 2747	2271 GTGTGTTTTGCACAGCACACCCCATCTCTTCCAGCAGAAAGT	. 2 .
	2270 2687	26	₽ ₹
	2627	2151 TTTCCTGTCATAATGTCAAAAGAATCTCAGA 	8 8
	2150 2567	25	გ ₹
		2031 ACCCTGGCTGCTGACGTTATGAGACCTCGAAGGAATGAY	₽ ₹
	2030 2447	1977 ATCCGATTAAATGGATACCCTTTCTTGGATGCAAAAGAAGAATTCACTCAT 	₽ ¥
	1976 2387	1917 GTCATGACCAGTAAATGGGTTGGAGATGCCTTTGGCAGGAAGGC	B X
	1916 2327	1857 GTGGTTATTGTTTTGAGCTTACTGGAGGCTTGGAATA: 	β _Σ
	1856 2267	1797 TATGCCATGGTTGGTGCTGCTGCATGCTTAGGT	A A
	1796 2207	1737 GACTGGTTTATCTTTAAGGAGTGGTGTGAGGTCGGGGCTGAT 	₽ ₹
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	1676 2087	1617 ACAGTATTCACTTTTGGCATCAAGGTTCCATCAGGCTTGTTCATCCCCAGCA 	8 8
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	1556 1967	1497 TACAGAAATGACATGAAATGCCAGTAAAATTGTCGATGACATTCCTGA 	유 첫
	1496 1907	1437 GAACTGATCAAAGAGCTTTTTACAGACTGTGGTCCCCTGGAATCCTCTTTCTCTTTTGTGA 	8 8
٠	1436 1847	1377 GTTGCAGCCATTACTGCTGTGATAGCCTTCCCTAATCCATACACTAG 	₽ ₹
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TGCTGCTTTGACAGTAAAGAGAA 3530	ATATACAAGTGCTGTTGAGCATAATTAAATAAAATGCT		V
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ATTGTGTGCCGTGTGGCTCAAAA 335 	AGGTAAAGTCTCGAAGGAAGCGAGAACGAAATCTCTC/	3291 3693	ДУ
ACCACAACAAAGGCTCATCAAAC 329 	TTGTACCATCACTAAATGCTTGGAACAGTACACATGC/	3231 3633	Qу Db
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AGCATTACCTTTCTACATTCCAG 305 	CAAAACTGTTCTGTTTAATTCATGAATTGTATAGTTAA 	ω ώ	Qу
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CACATTATCAGTCCCTATTTCTA 293 	CTCGAGCACCTGGCCTGTTGCTCAACATTGCAAAGAC	2871 3288	Qу Db
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		2808	Db

В

ATATACAAGTGCTGTTGAGCATAATTAAATAAAATGCTGCTGCTTTGACAGTAAAGAGAA 3932

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                                                  GGAACTCATTATACAATGACAATGGAGGCAGCATTAACAGTTCTACACATTTACTGGAT 296
TCAGCATGGGAAATGACAAAAAGTTTGTATGATGCGTGGTCAGGATGGCTAGTAGTAACA
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AF029346.1 G
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Submitted (09-OCT-1997) Physiology and Biophysics,
200 lst Street SW, Rochester, MN 55905, USA
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LTLPHMSGTANONGAGTMENN
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/tissue_type="lens epith
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Eutheria; Primates;
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                                   357
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                                                                                                                                                      237 GGAACTCATTATACAATGACAAATGGAGGCAGCATTAACAGTTCTACACACATTTACTGGAT
GGAACTCATTATACAATGACAAATGGAGGCAGCATTAACAGTTCTACACATTTACTGGAT
                                                                                                                                                                                                           2296;
                                                                  and Nelson,D.J.
and Nelson,D.J.
Regulation of human CLC-3 channels by multir
Ca2+/calmodulin-dependent protein kinase
r miol. Chem. 276 (23), 20093-20100 (2001)
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Huang,P., Liu,J., Di,A., Robinson,N.C., Musch,M.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission Submitted (27-JUL-1999)
                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Huang, P., Nissen, J., Johnson, X.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Molecular Identification
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AF172729.1 GI:5759223
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ang,P., Di,A., Kaetzel,M.A.,
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                                                                                                                                                                                                                                                                                             681
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RHRRINSKKKESAWEMYKSLYDAWSCWLVVTLTGLASCALAGLIDIAADWMTDLKEGI
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FILLGVFGGLWGAFFIRANIAWCRRKKSTKFGKYPVLEVIIVAAITAVIAFPNPYTRL
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LPARSPRPLKLRSILDMSPFTVTDHTPMEIVVDIFRKLGLRQCLVTHNGRLLGIITKK
LTILBHWAGANGCAGATATANI
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1. .2457
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                                                                                                                                                                                                        Score 2294.8;
Pred. No. 0;
0; Mismatches
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                                                                  279
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1419	360 GAACTGATCAAAGAGCTTTTTACAGACTGTGGTCCCCTGGAA	DЬ
1496	TGATCAAAGAGCTTTTTACAGACTGTGGTCCCCCTGGAATCCTCTTTCTCTTTGTGA	Qy
1359	w	рь
1436	377 GTTGCAGCCATTACTGCTGTGATAGCCTTCCCTAATCCATACACTAGGCTAAACACCAG	Qy
9		ρb
37	317 TGGTGTCGTCGACGCAAGTCCACGAAATTTGGAAAGTATCCCCGTTCTGGAAGTCATTATT	QV
ω	100 ATTCTTCTAGGGGTATTTGGAGGGCTTTGGGGAGCCTTTTTCATTAGGGCAAATATTGCC	망
1316	257 ATTCTTCTAGGGGTATTTGGAGGGCTTTGGGGGAGCCTTTTTCATTAGGGCAAATATTGC	Qγ
\vdash	120 CTGGTCCTTTTTATGTGGAGTATCATACACCATGGTACCTTTTTGAACTGTTTCCTTTT	Дb
1256	197 CTGGTCCTTTTTTATGTGGAGTATCATACACCATGGTACCTTTTTGAACTGTTTCCTTTT	Qy
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939		В
1016	57 AATATCTTTTCCTACCTCTTTCCAAAGTATAGCACAAACGAAGCTAAAAAAAA	Qy
879	20 GCATCAGGTTTGAGTTTAGGAAAAGAAGGTCCCCTGGTACATGTTGCCTGCTGCTGCGGA	В
956	97 GCATCAGGTTTGAGTTTAGGAAAAGAAGGTCCCCTGGTACATGTTGCCTGTTGCTGCGGA	Qy
		DЪ
896	37 AGAGGTTACTTGGGAAAATGGACTTTAATGATTAAAACCATCACATTAGTCCTGGCTGTG	Qy
759	700 CCATATGCCTGTGGCTCTGGAATTCCAGAGATTAAAACTATTTTAAGTGGATTCATCATC	Db
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699	40 TACATCTTCTGGGCCTTGAGTTTTGCCTTTCTTGCAGTTTCCCTGGTAAAGGTATTTGCT	Db
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	80 GCAGAATTAATCATAGGTCAAGCAGAGGGTCCTGGTTCTTATATCATGAACTACATAATG	В
716	CAGAATTAATCATAGGTCAAGCAGAGGGTCCTGGTTCTTATATCATGAACTACATAAT	Qy
579 ·	20 TGGGGATCTAATGAAACAACATTTGAAGAGAGGGATAAATGTCCACAGTGGAAAACATGG	рь
656	97 TGGGGATCTAATGAAACAACATTTGAAGAGAGGGATAAATGTCCACAGTGGAAAACATGG	Qy
519	60 ACTGACCTAAAGGACGCCATTTGCCTTAGTGCGTTGTGTACAACCACGAACAGTGCTGT	망
596	37 ACTGACCTAAAGGAGGGCATTTGCCTTAGTGCGTTGTGGTACAACCACGAACAGTGCTGT	Qy
536 459	477 CTAACAGGATTGGCATCAGGGGCACTGGCCGATTAATAGACATTGCTGCCGATTGGATG	Db Qy
399	40 TCAGCATGGGAAATGACAAAAAGTTTGTATGATGCGTGGTCAGGATGGCTAGTAACA	gb
7	17 TCAGCATGGGAAATGACAAAAAGTTTGTATGATGCGTGGTCAGGATGGCTAGGTAGTAACA	Qy

AATAATGTTCAACTGA 2534 	51 44	Qy Db
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ATTGCAATAGAAAGTGCCAGGAAAAAACAAGAAGGTATCGTTGGCAGTTCTCGGGTGTGT	2217 2140	Qy Db
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TACAGAAATGACATGAATGCCAGTAAAATTGTCGATGACATTCCTGATCGTCCAGCAGGC	1497 1420	Qy

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AUTHORS'
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ORGANISM
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VERSION
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AF029348
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Best Local Sim
Matches 2179;
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                                       CTTTTGGATGAACCAATTCCAGGTGTTGGTACATATGATGATTTCCATACTATTGACTGG 279
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AF029348
AF029348.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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Oryctolagus
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                                                                                                                                                                                              Similarity
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                                                                                                                                                                                  Conservative
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LPAESSPRPLKLRSILDMSPFTVDHTPMEIVVDIFRKLGLRQCLVTHNGRLLGIITKK
DLIRHMAQTANQDPASIMFN"
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complement(2429...2457)
/note="PCR primer designed from human GenBank Accession Number X78520"
a 468 c 593 g 727 t
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/db_xref="taxon:9986"
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and Shepard, A.R.
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                                       AGGAACTCATTATACAATGACAAATGGAGGCAGCATTAACAGTTCTACACATTTACTGGA 295
Direct Submission
Submitted (31-AUG-1993) Masanobu Kawasaki, Tokyo Medical and Dental
University, Second Department of Internal Medicine; 1-5-45 Yushima,
Bunkyo-ku, Tokyo 113, Japan (Tel:03-3813-6111, Fax:03-3818-7177)
Submitted (31-Aug-1993) to DDBJ by:
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CLC family; protein kinase C-regulated chloride
pattus rattus kidney cDNA to mRNA, clone ClC-3.
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/protein_id="BAA04471.1"
/db_xref="GI:699624"
/db_xref="GI:699624"
/translation="mYNNGGSINSSTHLLDLLDEPIPGVGTYDDFHTIDWVREKCKDRE
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03-3818-7177.
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639 c 763 g
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499. .2781
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Rattus rattus"
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                                                                                                                                                 58.1%;
92.4%;
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Rodentia;
                                                                                                                           Score 2104.8;
Pred. No. 0;
0; Mismatches
                                                                                                                               0;
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                                                                                                                               182;
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GTGATAGCCTTCCCTAATCCATACACTAGGCTAAACACCAG 1435 	TGTTGCAGCCAFTACTGCTGTGATAGCCTTCCCT	1376 1623	ОУ
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TCTTTTTAGCCTGGAGAGAGGTTAGCTATTATTTTCCTCTCAAAACTTTATGGAGATCATT 1135 	TCTTTTAGCCTGGAAGAC	1076 1323	ОУ
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 GTACATCTTCTGGGCCTTGAGTTTTGCCTTTCTTGCAGTTTCCCTGGTAAAGGTATTTGC 775 	GTACATCTTCTGGGCCTTC + + + + + + + + + + + + + + + + + + +	716 963	Qy Db
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GC 2	CATTATAACAAAAAAAGATATCCTCCGTCATATGGCCCAGACGCAAACCAAGACCCCG	2703	Db
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66 -	TTCCGAAAGCTTGGTCTGAGGCAGTGCCTTGTCACTCACAATGGGCGCCTCCTT	2643	Db
66	тттссвалавствевастваевсявтвесттвталстследатвевсесстсстт	2396	Qу
GA -	CCTTTTACAGTGACAGACCACACCCCAATGGAGATTGTGGTA	2,583	Db
GA	ATTCTTGACATGAGCCCTTTTACAGTGACAGACCACACCCCAATGGAGATTGTGGTG	2336	Qy
8 -		52	Db
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AC -	ATAATGTCAAAAGAATCTCAGAGATTAGTGGGATTTGCCCTCAGAAGAGACCTG	2403	Db
AC	GTCATAATGTCAAAAGAATCTCAGAGATTAGTGGGATTTGCCCTCAGAAGAGACCTG	2156	Qy
ි <u>-</u>	AATATGACAGTAGATGACATAGAAAACATGATTAATGAGACCAGCTATAATGGCT	2343	Db
- 유	CAATATGACAGTGGATGATATAGAAAACCATGATTAATGAAACCAGCTACAATGGATTTC	2096	Qy
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G =	CCGACTAAATGGGTACCCTTTCTTGGATGCAAAAGAAGAATTCACTCATACAACC	2223	Db
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6C =	GTGGTTATTGTTTTTGAACTTACTGGAGGCTTGGAATATATTGTTCCTCTTATGGCTG	2103	DЪ
<u>.</u> ප	GTGGTTATTGTTTTTGAGCTTACTGGAGGCTTGGAATATATTGTTCCCCCTTATGGC	1856	Qy
CH =	GCATGCTTAGGTGGTGTGACAAGAATGACTGTCTCT	2043	DЪ
CH	ATGCCATGGTTGGTGCTGCTGCATGCTTAGGTGGTGTGACAAGAATGACTGTCTCC	1796	Qy
Ğ-	CGACTGGTTCATCTTCAAGGAGTGGTGTGAGGTCGGGGCTGACTGCATCACTCCTGGG	1983	Db
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CA =	CGGAGCCATTGCAGGGAGTTGTGGGGGATTGCTGTGGAGCAGCTCGCCTACCACC	1923	рь
CA	GAGCGATCGCAGGAAGGATTGTGGGGATTGCGGTGGAGCAGCTTGCCTACTATCAC	1676	Qy
AT.	GACAGTATTCACTTTTGGTATCAAGGTCCCGTCGGGCCTGTTTATCCCCAGCATGGCG		Db
ΑŢ	ACAGTATTCACTTTTGGCATCAAGGTTCCATCAGGCTTGTTCATCCCCAGCATGGCC	1616	Qy
AT	CGTTGGAGTATATTCAGCTATCTGGCAGTTGTGCCTAGCACTCATATTTAAAATAATA	1803	Db
ΑŢ	ATTGGAGTATATTCAGCTATATGGCAGTTATGCCTGGCACTCATATTTAAAATCATA	1556	Qy
୍ର -	AAATGACATGAATGCCAGTAAAATTGTTGATGATATTCCTGACCGACC	1743	Db
- 6	TACAGAAATGACATGAATGCCAGTAAAATTGTCGATGACATTCCTGATCGTCCAGCA		Qy
GA -	TAAAGAGCTGTTTACAGACTGTGGCCCCTTGGAATCCTCCTCTTTGT	1683	Db
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DB 10;

Length

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FEATURES
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AUTHORS
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2 (bases 1 to 2758)
Borsani,G., Rugarli,E.I., Taglialatela,M., Wong,C. and Ballabio, Characterization of a human and murine gene (CLCN3) sharing similarities to voltage-gated chloride channels and to a yeast integral membrane protein genomics 27 (1), 131-141 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MMCLCN5 2758
M.musculus mRNA for Clcn3.
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Institute for Molecular
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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376. . . 2658
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                           TTTTGCACAGCACACCCCATCTCTTCCAGCAGAAAGTCCTCGGCCATTGAAGCTTCGAAG
                                                    AATTGCAATAGAAAGTGCCAGGAAAAAACAAGAAGGTATCGTTGGCAGTTCTCGGGTGTG
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Reno, NV 89557, USA
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Direct Submission
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Reno, NV 89557, USA
3 (bases 1 to 2305)
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Direct Submission
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Cavia porcellus
Eukaryota; Metazoa;
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LSFAFLAVSLVKVFAPYACGCGNIFSYLFPKYSTNEAKKEVLSAASAAGVSVAFGAPTGGVL
FSLEEVSYYFPLKTLGRSFFAALVAAFVLRSINPGNSRLVLFYVEYHTPWYLFELFF
FILLGVEGGLWGAFFIRANIAWCRRRSTKFGKYPVLEVIIVAAITAVIAFPNPYTRL
NTSELIKELFTDCGPLESSSLCDYRNDMNASKIVDDIPDRPAGVGVYSAIWQLCLALI
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/db_xref="taxon:10141"
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	TT 1205	6 TTAGTGGCTGCATTTGTTTTGAGGTCCATCAATCCATTTGGTAACAGCCGTCTGGTCC	1146	Qy
	CT 900	1 CTGGAGGAGGTTAGCTATTATTTTCCTCTTAAAACTTTAGGGAGATCATTTTTTTGCTGCT	4- 0	B 3
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	10	6 GCCTCAGCTGCAGGGGTTTCTGTAGCTTTTTGGTGCACCAATTGGAGGAGTTTCTTTTTAGC	1026	P 09
	CT 1025	6 TCCTACCTCTTTCCAAAGTATAGCACAAACGAAGCTAAAAAAAGGGAGGTGCTATCAGC 	966 721	Оу
	TT 965	16 TIGAGTITAGGAAAAGAAGGTCCCCTGGTACATGTTGCCTGTTGCTGCGGAAATATCTTT 	906 661	QУ.
	CAGGT 905	6 TTGGGAAAATGGACTTTAATGATTAAAACCATCACATTAGTCCTGGCTGTGGCATO 	846 601	Оу
	AC 845	16 TGTGGCTCTGGAATTCCAGAGATTAAAACTATTTTAAGTGGATTCATCATCATCAGAGGTTAC	786 541	оу Оу
	3CC 785 	6 TGGGCCTTGAĞTTTTGCCTTTCTTGCAGTTTCCCTGGTAAAGGTATTTGCTCCATATGCC 	726 481	Qу рь
	TTC 725	6 ATCATAGGTCAAGCAGAGGGTCCTGGTTCTTATATCATGAACTACATAATGTACATC 	666 421	Qу Дъ
:	TA 665	16 AATGAAACAACATTTGAAGAGAGGGATAAATGTCCACAGTGGGAAAACATGGGCAGAATTA 	606 361	Qу
	CT 605	6 AAGGAGGGCATTTGCCTTAGTGCGTTGTGGTACAACCACGAACAGTGCTGTTGGGGATCT 	546 301	Ф
	TA 545	16 TTGGCATCAGGGGCACTGGCCGATTAATAGACATTGCTGCCGATTGGATGACTGAC	486 241	Qу
	CAGGA 485	6 GAAATGACAAAAAGTTTGTATGATGCGTGGTCAGGATGGCTAGTAGTAACACTAAC 	426 181	Фр
	1GG 425 	16 AAATGTÄÄAGACAGAGAAAGGCATAGACGGATCAACAGCAAAAAGAATGAGCATCAGCATCG 	366 121	QУ
	AA 365 AG 120)6 GAACCAATTCCAGGTGTTGGTACATATGATGATTTCCATACTATTGATTG	306 61	Фр
v	GAT 305 GAT 60	6 TATACAATGACAAATGGAGGCAGCATTAACAGTTCTACACATTTACTGGATCTTTTGG	246 1	рь
0; .	Gaps	Match 57.8%; Score 2095.4; DB 10; Length 2305 cocal Similarity 94.3%; Pred. No. 0; s 2174; Conservative 0; Mismatches 131; Indels 0;	uery Mat est Loca atches 2	Qu Be Ma
I EN T PS TKK	AVMTSKWVG 'QDNMTVDD 'SRVCFAQH INGRLLGII	DCITPGLYAMVGAAACLGGVTRMTVSLVVIVFELTGGLEYIVPLMAAVMTSKWVGDAGREGIYEAHIRLNGYPFLDAKEEFTHTTLAADVMRPRNNDPPLAVLTQDNMTVDDIE MINETSYNGFPVIMSKESQRLVGFALRRDLTIAIESARKKQEGIVGSSRVCFAQHTPLLPAESPRPLKLRSILDMSPFTVTDHTPMEIVVDIFRKLGLRQCLVTHNGRLLGIITKLDIITMSCARMAQTANQDDASIMFN" 627 a 442 c 552 g 684 t	H	BASE

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26 GAAAGTGCCAGGAAAAAACAAGAAGGTATCGTTGGCAGTTCTCGGGTGTGTTTTGCACAG 2285	CAAAAGAATCTCAGAGATTAGTGGGATTTGCCCTTAGAAGAGACTTGACAATTGCAA	6 TCAAAAGAATCTCAGAGAATTAGTGGGATTTGCCCTCAGAAGAGAGACCTGACA	1 GTGGACGACATAGAAAACATGATTAATGAAACCAGCTACAATGGCTTTCCTGTCA	6 GTGGATGATATAGAAAACATGATTAATGAAACCAGCTACAATGGATTTCCTGTCATAAT		6 GTTATGAGACCTCGAAGGAATGATCCTCCCTTAGCTGTCCTGACACAGGACAATATGAC	1 AATGGATACCCTTTCTTGGATGCAAAAGAAGAATTTACTCATACCACCCTGGCTGC	6 AATGGATACCCTTTCTTGGATGCAAAAGAAGAATTCACTCATACCACCCTGGCTGCTG	1 AGTAAATGGGTTGGAGATGCCTTTGGTAGAGAAGGCATCTATGAAGCACACATCCGT	6 AGTAAATGGGTTGGAAGATGCCTTTGGCAGGGAAGGCATTTATGAAGCACACACCGATT	1 GTTTTTGAACTTACTGGAGGCTTGGAATATATTGTACCTCTTATGGCTGCAGTAATG	6 GTTTTTGAGCTTACTGGAGGCTTGGAATATATTGTTCCCCTTATGGCTGCAGTCATGAC	1 GTTGGTGCTGCGTGCGTTAGGTGGCGTGACAAGGATGACTGTCTCCCTGGTGGT	6 GTTGGTGCTGCATGCTTAGGTGGTGTGACAAGAATGACTGTCTCCCCTGGTGGTTAT	01 ATCTTTAAGGAGTGGTGTGAGGTTGGGGCTGATTGCATTACACCCGGCCTTTATGCCATG 1560	6 ATCTTTAAGGAGTGGTGTGAGGTCGGGGCTGATTGCATTACACCTGGCCTTTTATGCCAT		6 GCAGGAAGGATTGTGGGGATTGCGGTGGAGCAGCTTGCCTACTATCACCACGACTGGTT	1 ACTITCGGCATCAAGGTTCCATCAGGCTTGTTCATCCCCAGCATGGCCATTGGAGCAAT	6 ACTITIGGCATCAAGGTTCCATCAGGCTTGTTCATCCCCAGCATGGCCATTGGAGCG	1 TATTCAGCTATATGGCAGTTATGCTTAGCACTATTTAAAATCATAATGACAGTATT	6 TATTCAGCTATATGGCAGTTATGCCTGGCACTCATATTTAAAATCATAATGACAGTAT	1 GACATGAATGCCAGT	6 GACATGAATGCCAGTAAAATTGTCGATGACATTCCTGATCGTCCAGCAGGCATTGGAGT	01 AAAGAGCTTTTCACAGACTGTGGTCCCCTGGAATCCTCTTCTCTGTGTGACTACCGAAAT 1260	6 AAAGAGCTTTTTACAGACTGTGGTCCCCTGGAATCCTCTTCTCTTTTGTGACTACAGAAA		6 ATTACTGCTGTGATAGCCTTCCCTAATCCATACACTAGGCTAAACACCAGTGAACTG	1 CGACGCAAGTCCACCAAATTTGGAAAGTATCCTGTTCTTGAAGTCATTATTGT	6 CGACGCAAGTCCACGAAATTTGGAAAGTATCCCCGTTCTGGAAGTCATTATTGTTGCAGC		6 GGGGTATTTGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	61 TTTTATGTGGAGTATCATACACCATGGTACCTTTTTGAATTGTTTCCTTTATGTCTTTATGTCTCTCTC		

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Cavia porcellus chloride channel Clc-3 (CLCN3) mRNA, complete cds.
AF133214
AF133214.1 GI:4928465
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DCITPGLYAMVGAAACLGGVTRMTVSLVVIVFELTGGLEYIVPLMAAVWTSKWVGDAF
GREGIYFGAHTBINGVDETAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="ion channel; similar to Cavia porcellus CLC-3 encoded by GenBank Accession Number U83464; similar to the Homo sapiens product encoded by GenBank Accession Number
                         GREGIYEAHIRLNGYPFLDAKEEFTHTTLAADVMRPRRNDPPLAVLTQDNMTVDDIEN
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LPAESPRPLKLRSILDMSPFTVTDHTPMEIVVDIFRKLGLRQCLVTHNGRLLGIITKK
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Qy 115	Qy 10 .Db 8	Qy 10 Db 7	Qy 9 Db 7	Qy 9 Db 6	Qy 8	Qy 7 Db 5			Оу 6 	. Qy 5	Qy 4 Db 2	Qy 4 . Db 1	Qy 3 Db 1	Qy 3 Db	Qy 2 Db	Query Best Match	BASE CC ORIGIN
52 GCTGCAT	92 GAGGTT	32 81	72 21	12 61	52 AAATO 01 AAGTO	92 TC:	32 TT 81 TT	72 GGTCAAGC	12	52	92 TCAGO 41 TCAGO	32 81	72 AA 21 AA	112 ATTCC 61 ATTCC	1	ery Match st Local Si ches 2159;	COUNT
	8-8	AGGGGTTT(AGGTGTTTC	TCCAAAGT! TCCAAAGT!	AAAAGAAG(AAAAGAAG(GACTTT GACTTT	FGGAATTCCAG <i>I</i> FGGAATTCCAG <i>I</i>	TTTTGCCT:	AGCAGAGG(ATTTGAAGA ATTTGAAGA	TTGCCTTAC	GGCACTGGCC	ACAAAAGTTTGTATGATGCG	CAGAGAAA(CAGAGAAA(AGGTGTTGO	ATGACAAATGGAGGCF	milarity Conserv	619 a
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TCAATCCATTTG	CTATTATTTCCTCTCAAAACTTTATGGAGATCATTTTTG 	GCTGCAGGGGTTTCTGTAGCTTTTGGTGCACCAATTGGAGGAGTTCTTTTAGCCTG 	CTCTTTCCAAAGTATAGCACAAACGAAGCTAAAAAAAAGGGAGGTGCTATCAGCTGCCTC 	TACATGTTO	AATGATTAAAACCATCACATTAGTCCTGGCTGTGGCAT 	AGAGATTAAAACTATTTTAAGTGGATTCATCATCAGAGGTTACTTG 	GAGTTTTGCCTTTCTTGCAGTTTCCCTGGTAAAGGTATTTGC 	AGAGGGTCCTGGTTCTTATATCATGAACTACATAATGTACATCTTC 	ACAACATTTGAAGAGAGGGATAAATGTCCACAGTGGAAAACATGGGCAGAATTAATC 	GGTACAACC GGTATAACC	attaatagacattgctgccgattggatgactgacctaa 	GTGGTCAGGATGGCTA ATGGTCAGGATGGCTT	AGACAGAGAAAGGCATAGACGGATCAACAGCAAAAAGAAAG	ATTCCAGGTGTTGGTACATATGATGATTTCCATACTATTGATTG	agcattaacagtictacacatttactggatcttttggat 	Score 2 Pred. N 0; Mism	546 g
3TAA(TATGGAGA	CAATTGGA CGATTGGA	\AAAAAAAGG \AAAAAAAGG	CCTGTTGC	TAGTCCTG	AGTGGATTC AGTGGATTC	STAAAGGTA STAAAAGTA	ATGAACTAC ATGAATTAT	CAGTGGAAA CAGTGGAAA	CACGAACAG CATGAACAG	SCTGCCGAT	rggctagta ggcttgta	AGCAAAAAG AGCAAAAAG	CATACTATT	ACACATTTA ACACACTTA	2084.6; No. 0; matches	679 t
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STCTGGTCCTTT	TGCTGCTTTAGTG	TTTTAGCC: TTTTAGCC:	ATCAGCTGO	ATGTTGCCTGTTGCTGCGGAAATATCTTTTCCTAC 	CAGO 111 CAGO	AGGTTACT	ATGCC1	CATCTTCTG	AGAATTAA' AGAATTAA'	GGGATCTA. GGGATCTA!	TGACCTAAA TGATTTAAA	AACAGGAT!	AGCATGGG. AGCATGGG.		TTTGGATG. TTTGGATG	Length 2:	
TTTAT 1	TAGTG 11 TAGTA 90	TGGAA 1	CCTCA 1	CCTAC 97 CCTAC 72	STTTGAGT 911 SCTTGAGT 660	TGGGA 851 TGGGA 600	NGTGGC 7,9	GGGCC 731 GGGCC 480	TCATA 6	VATGAA 61 VATGAA 36	AGGAG 5	TTGGCA 49	AAATG 43 AAATG 18	AAATGT 37 SAAGTGT 12	rgaacca 3 rgaaccg 6	283; 0; Gap	

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ACTTTATGGAGATCATTT 1136		STTGCCTGCTGCGA 1084 SCTAAAAAAAGGGGGGTG 1016		TGGTAAAGGTATTTGCT 776	CCACAGTGAAAACATGG 784 ATCATGAACTACATAATG 716	AACCACGAACAGTGCTGT 596	IIIIIII IIIII IIIIII IIIIIIIIIII		TCCACACACTTGCTGGAT 424 TCCACACACTTGCTGGAT 356	10; Length 2659; 3; Indels 0; Gaps 0; TCTACACATTTACTGGAT 296	VDIFRKLGLRQCLVTHNGRLLGIITKK
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7 ATTGCAATAGAAAGTGCCAGGAAAAAACAAGAAGGTATCGTTGGCAGTTCTCGGGTGTGT 22	221	S S
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7 TATGCCATGGTTGGTGCTGCATGCTTAGGTGGTGTGACAAGAATGACTGTCTCCCTG 18	179	8
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7 GACTGGTTTATCTTTAAGGAGTGGTGTGAGGTCGGGGCTGATTGCATTACACCTGGCCTT 17		_S
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5 ACAGTATTCACTTTTGGTATCAAGGTCCCGTCGGGCCTGTTTATCCCCAGCATGGCGATC 18	174	. <u>D</u>
7 ACAGTATTCACTTTTGGCATCAAGGTTCCATCAGGCTTGTTCATCCCCAGCATGGCCATT 16	161	, Q
5 GTTGGAGTATATTCAGCTATCTGGCAGTTGTGCCTAGCACTCATATTTAAAATAA		₽.
7 ATTGGAGTATATTCAGCTATATGGCAGTTATGCCTGGCACTCAT	,	Qy
25 TACAGAAATGACATGAATGCCAGTAAAATTGTTGATGATATTCCTGACCGACC	162	₽
7 TACAGAAATGACATGAATGCCAGTAAAATTGTCGATGACATTCCTGATCGTCCAG	149	õ
55 GAACTGATTAAAGAGCTGTTTACAGACTGTGGCCCCCTTGGAATCCTCCTCTCTTTGTGAC 1624		D)
7 GAACTGATCAAAGAGCTTTTTACAGACTGTGGTCCCCTGGAATCCTCTTCTCTTTTGTGAC 14	143	8
5 GTTGCAGCCATTACTGCTGTGATAGCCTTCCCCAACCCCATACACAAGGCTCAACACGGT 15	-	Db
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AF029347.1 GI:2599549
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Direct Submission
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LSFAFLAVSLVKVFAPYACGSGIPEIKTILGSFIIRGYLGKWTLMIKTITLYLAVASG
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FSLEEVSYYFPLKTLWBSFFAALVAAFVLRSINPFGNSRLVLFYVEYHTPWYLFELFP
FILLGVFGGLWGAFFIRANIAWCRRKCTKFGKYPVLEVIIVAATTAVIARPNPYTRL
NTSELIKELFTDCGPLESSSLCDYRNDMNASKIVDDIPDRPAGVGVYSAIWQLCLALI
FKILMTVFTFGIKVPSGLFIBSMAIGALAGRIVGIAVYBCLAXYHLDWFIRKEWCEVGA
DCITPGLYAMVGAAACLGGVTRMTVSLVVIVFELTGGLEYIVPLMAAVMTSKWVGDAF
GREGIYEAHIRLNGYPFLDAKEEFTHTTLAADVVRAPRRSDPPLAVLTQDNNTVDDIEN
MINETSYNGFPVIMSKESORLVGFALRRDLTIAIESARKKOEGIVGSSRVCFAQHTPS
LPAESSPRPLKLRSILDMSPFTVYDHTPMEIVVDIFRKLGLRQCLVTHNGRLLGIITKK
DILRHMAQTANQDPASIMFN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Street SW, Rochester, Location/Qualifiers
 a
/note="PCR primer designed from human
GenBank Accession Number X78520"
a 493 c 610 g 699 t
                                     /note="PCR primer designed from GenBank Accession Number X78520" complement(2429. .2457)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and Shepard, A.R
                                                                                                                                                                                                                                                       /translation="meseQlfHrgyxrnsynsITsassDeelldgagaImDfQTSeDD
NLLDGDTAAGTHYTMTNGGSINSSTHLLDLLDEPIPGVGTYDDFHTIDMVREKCKDRE
RHRRINSKKKESAWEMTKSLYDAWSGWLVVTLTGLASGALAGLIDIAADWMTDLKEGI
                                                                                                                                                                                                                                                                                       /product="chloride channel
/protein_id="AAB95162.1"
/db_xref="GI:2599550"
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/product="chloride
                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
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/tissue_type="lens epit
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Submitted (22-DEC-1999)
Laboratoire Jean Maetz,
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Lindenthal, S.M.B.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (04-DEC-1996) S.M.B. Lindenthal, Physiologie Des Membranes, La Darse - B.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopus laevis.
Xenopus laevis
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Lindenthal,S.M.B.
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VLRSIAPFGNSRLVLFYVEYHPWYLFELIPFILLEVGGLWGAFFIRANIAWCRRK
VLRSIAPFGNSPLVEVIAVAAITAIIAFPNPYTRENTSQLIKETDCGPLESSSLCDVAYKND
STRFGRYPVLEVIAVAAITAIIAFPNPYTRENTSQLIKETDCGPLESSSLCDKAYKND
MNASKIVDDIEDRPAGTGVYSAIWOLCLALVFKIIMTVETFGIKVPSGLFIPSMAIGA
IAGRIVGIAVEQLAYYHHDWFIFKEWCEVGADCITPGLYAMVGAAACLGGVTRMTVSL
VVIVFELTGGLEYIVPLMAAVMTSKWVGDAFGREGIYEAHIRLNGYPFLDAKEEFTHT
                                                                                                                                                                      /translation="MDISSDPYLPYDGGGDNIPLRDLHKRGTHYTVTNGGAINSTTHL
LDLLDEPIPGVCTYDDPHIDWVREKCKDRERHERINSKKESAMELAKSLYDAWSGW
LVLTLTGLASGALAGFIDIAADWADLKEGICWTAFWFHEQCCWDSKEATFEERDKC
PQWQTWADLIIQAEGPGSYINNYFMYLFWALSFAFLAYCLVKVFAPYACGSGIPEIK
TILSGEIIRGYLGKWTLMIKTITLVLAVASGLSLGKEGPLVHVACCCGNIFSYLFFKY
                  MEIVVDIFRKLGLRQCLVTHNGRLLGIITKKDILRHMAQMANHDPESILFN"
                                 TLARDVMRPRRNDPPLAVLTQDDMTVDDVESLINDTSYNGFPVIMSKESQRLVGFALR
RDLTLAIENARKKQDGIVGSSRVCFAQHTPSLPAESPRTLKLRSILDMSPFTVTDQTP
                                                                                                                                                                                                                                                              /product="putative chloride channel ClC-3"
/protein_id="CAA71072.2"
/db_xref="GI:6634696"
/db_xref="SPTREMBL:Q9YH11"
                                                                                                                                                                                                                                                                                                                                                                                      /organism="Xenopus laevis"
/db_xref="taxon:8355"
/cell_line="A6"
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Location/Qualifiers
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238, Villefranche
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                              ACATTAGTCCTGGCTGTGGCATCAGGTTTGAGTTTAGGAAAAGAAGGTCCCCTGGTACAT
                                                                                                                                                              CTGGTAAAGGTATTTGCTCCATATGCCTGTGGCTCTGGAATTCCAGAGAITAAAACTATT
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ACATTATGGAGATCATTCTTTGCAGCCTTAGTAGCAGCATTTGTTCTAAGGTCAATTAAC
                                                                                                                                                                                              CTTGTGAAAGTATTTGCCCCCTTATGCTTGTGGTTCAGGAATACCAGAGATTAAAACTATT
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79.1%;
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	131 CTCAGAAGAGATTTGACATTAGCCATTGAAAATGCAAGAAAAAAGCAAGATGGTATTGTT	Дb
2258	CTCAGAAGAGACCTGACAATTGCAATAGAAAGTGCCAGGAAAAAAACAAGGAAGG	Qy
2130		Db.
2198 .	GCTACAATGGATTTCCTGTCATAATGTCAAAAGAATCTCAGAGATTAGTGGGATTTGCC	Оу
2070		Db
2138	079 GCTGTCCTGACACAGGACAATATGACAGTGGATGATATAGAAAACATGATTAATGAAACC	Qy
2010	1951 TTCACACATACAACTCTAGCTCGTGATGTGATGAGACCAAGAAAGA	Дb
2078	019 TTCACTCATACCACCCTGGCTGCTGACGTTATGAGACCTCGAAGGAATGATCCTCCCTTA	Qy
1950	891 GGTATATATGAAGCTCATATACGGCTGAATGGATATCCATTTTTGGATGCCAAGGAGGAA	Дb
2018	959 GGCATTTATGAAGCACACATCCGATTAAATGGATACCCTTTCTTGGATGCAAAAGAAGAA	Qy
1890	831 GTCCCCCTTATGGCAGCAGTGATGACCAGTAAGTGGGTTGGGGATGCCTTTGGAAGGGAA	DЬ
1958	899 GTTCCCCTTATGGCTGCAGTCATGACCAGTAAATGGGTTGGAGATGCCTTTGGCAGGGAA	Qy
1830	771 CGGATGACAGTCTCTTGTAGTCATAGTATTTGAGCTAACTGGGGGCCCTGGAATACATT	Дb
1898	839 AGAATGACTGTCTCCCTGGTGGTTATTGTTTTTGAGCTTACTGGAGGCTTGGAA1	Qy
	11 TGTATAACTCCTGGGCTATATGCTATGGTTGGTGCTGCTGCATGTCTTGGTGGTGTGAACC	Db
1838	779 TGCATTACACCTGGCCTTTATGCCATGGTTGGTGCTGCTGCATGCTTAGGTGGTGTGF	Qy
1710	o.	ДЪ
1778	719 CTTGCCTACTATCACCACGACTGGTTTATCTTTAAGGAGTGGTGTGAGGTCGGGGCTGAT	Qy
1650	591 ATCCCAAGCATGGCAATTGGTGCCATAGCAGGCCGGATTGTGGGCATTGCAGTGGAACAA	Db
1718	659 ATCCCCAGCATGGCCATTGGAGCGATCGCAGGAAGGATTGTGGGGATTGCGGTGGAGCAG	Ωγ
é	1 GTGTTCAAGATTATTATGACAGTCTTCACCTTTGGCATTAAGGTACCTTCAGGTCTGTT	Db
1658	599 ATATTTAAAATCATAATGACAGTATTCACTTTTGGCATCAAGGTTCCATCAGGCTTG	Qy
1530	1471 CCTGACCGCCTGCAGGGACTGGGGTGTACTCAGCTATTTGGCAGCTGTGCCTTGGCTCTG	Db
1598	539 CCTGATCGTCCAGCAGGCATTGGAGTATATTCAGCTATATGGCAGTTATGCCTGGCAC	Qy ,
1470	4	Db
1538	479 TCCTCTTCTTCTTGTGACTACAGAAATGACATGAATGCCAGTAAAATTGTCGATGACATT	Qy
41	51 ACACGGTTCAACACTAGCCAGTTGATAAAGGAGTTATTTACAGACTGTGGGCCTTTAGAA	Db -
1478	419 ACTAGGCTAAACACCAGTGAACTGATCAAAGAGCTTTTTACAGACTGTGGTCCCCTGGAA	0γ
1350	291 GTATTGGAGGTTAT	Db
1418	TICTGGAAGTCATTATTGTTGCAGCCATTACTGCTGTGATAGCCTTCCCTAATCC	Qy
1290	1231 ATCCGTGCGAATATTGCCTGGTGCCGGCGCGCAAATCAACCAGATTTGGGAGGTATCCA	Db
1358	299 ATTAGGGCAAATATTGCCTGGTGTCGTCGACGCAAGTCCACGAAATTTGGAAAGTATC	Qy
1230	71 TTTGAACTTATCCCATTTATTCTACTGGGTGTATTTGGAGGACTTTGGGGAGCGTTTTTC	Db
1298	239 TTTGAACTGTTTCCTTTATTCTTCTAGGGGGTATTTGGAGGGCCTTTGGGGAGCCCTTTTTC	Qy
1170	1111 CCTTTTGGAAACAGCCGTCTTGTCCTTTTCTATGTAGAATATCATACCCCATGGTATTTG	Db
1238	CATTTGGTAACAGCCGTCTGGTCCTTTTTTTATGTGGAGTATCATACACCATGGTACCTT	Qy

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PUBMED
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AUTHORS
TITLE
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ORGANISM
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Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
Labroidei; Cichlidae; Oreochromis.

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Rattus norvegicus
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Mammalia; Eutheria; )
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WEFIKSLLDAWSGWVWMLLIGLLAGTLAGVIDLAVDMWTDLKESVCLSAFWYSHEOCC
WTSORTFEDERORCPLWGKWSELLSQSEGASQVILNUWYILWALLFAFLAVSLVRV
FAPYACGSGIPEIKTILSGFIIRGYLGKWTLLIKTVTLVLVVSSGLSLGKEGPLVHVA
CCCGNFFSSLFSKYSKNEGKREVLSAAAAACVSVAFGAPIGGVLFSLEEVSYYFPLK
TLWRSFFAALVAAFTLRSINPFGNSRLVLFYVEYHTPWMAELFPFILLGVFGGLWGT
VFTRCNIAWCRRRKTTRIGKYPVLEVIVVTAITAIIAYDNPYTRQSTSELISELFNDC
GALESSGLCDYIMDPNWTRPVDDIPDRPAGVGVYTANWGLALFKIVITITFTFGNK
IPSGLFIPSMAVGAMAGRMVGIGVEDLAVHHDWIIFRTMCRPGADCVTPGLYAMVGA
AACLGGVTRMTVSLVVIMFELTGGLEYIVPLMAAAVTSKWVADAFGKEGIYEAHIHLN
GYPFLDVKDEFTHRTLATDWARPRRGBPPLSULTOSSMYNDDWTLKETDYNGFPVV
VSRDSERLIGFAQRRELILAIKNARQRQEGIVSNSIMYFTEEPPELPANSPHPLKLRR
ILNLSSFTVTDHTPMETVVDIFRKLGLRQCLVTRSGRLLGIITKKDVLRHMAQMANQD
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/db_xref="GI:555932"
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292 TGGATCTTTTGGATGAACCAATTCCAGGTGTTAGTILIIIIIIIIIIIIIIIIIIIIIIIIIIII
292 TGGATCTTTTGGATGAACCAATTCCAGGTGTTGGTAC
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192 TGGATCTTTTGGATGAACCAATTCCAGGTGTTAGTIA
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992 TGGATCTTTTGGATGAACCAATTCA
92 TGGATCTTTTGGATGAACCAATTCCAGGTGTTGGTA

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96158876
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Submitted (30-AUG-1995) I.W. Craig, University of Oxford, Genetics
Laboratory, Dept.of Biochemistry, South Parks Road, Oxford OX1 3QU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 3173)
Fisher, S.E., van Bakel, T., Lloyd, S.E., Pearce, S.H., Thakker, R.V. and Craig, I.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Lloyd, S.E., Pearce, S.H.S., Fisher, S.E., Steinmeyer, K., Schwappach, B., Scheinman, S.J., Harding, B., Bolino, A., Scodyer, P., Rigden, S.P.A., Wrong, O., Jentsch, T.J., Cra
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                                                                                                                                                                                                                                                                                                                                                       sequences
FAPYAOGSGIPEIKTILSGFIIRGYLGKWTLVIKTITLVLAVSSGLSLGKEGPLVHVA
CCCGNIICHCFNKYRKBEAKRREVLSAAAAGVSVAFGAPIGGVLFSLEEVSYFPLK
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LFIRTNIAWCRKRKTTQLGKYPVIEVLVVTAITAILAFPNEYTRMSTSELISELFNDC
                                                                                                                                                                                                              /clone_
292. .2
                                                    /db_xref="SWISS-PROT:P51795"
/translation="MDFLEEPIPGVGTVDFNTIDWVREKSRDRDRHREITNKSKESTVtranslation="MDFLEEPIPGVGTVDFNTIDWVREKSRDRDRHREITNKSKESTWALLHSVSDARSGWLLMLIGLISGSLAGLIDISAHWMTDLKEGICTGGFWFNHEHCCWALLHSVSDARSGWLALLIGLTSTDEGAFAYIVNYFMYVLWALLFAFLAVSLVKVWNSEHYTFEERDKCPEWNSWSQLIISTDEGAFAYIVNYFMYVLWALLFAFLAVSLVKV
                                                                                                                                                                                 /gene="CLCN5"
292. .2532
                                                                                                          /product="voltage-gated chloride
/protein_id="CAA63000.1"
/db_xref="GI:1171562"
                                                                                                                                                     /codon_start=1
                                                                                                                                                                                                                             /tissue_type="kidney"
/clone_lib="Clontech
                                                                                                                                                                                                                                                                                              /Organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                       equences X81836 and Location/Qualifiers
                                                                                                                                                                      /gene="CLCN5"
                                                                                                                                                                                                                                                         /clone="RL.3,
                                                                                                                                                                                                                                                                      /map="pl1.2;
                                                                                                                                                                                                                                                                                    /chromosome="X"
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ACLGGVTRMTYSLVVIMFELTGGLEYIYPLMAAAMTSKWVADALGREGIYDAHIRUNG
YPFLEAKEEEAHKTLAMDVMKPRRNDPLLTVLTQDSMTYEDVETIISETTYYSGPPVV
SRESQRLVGFVLRRDLIISIENARKKQDGVVSTSIIYFTEHSPPLPPYTPPTLKLRNI
                                                                                                                         LDLSPFTVTDLTPMEIVVDIFRKLGLRQCLVTHNGRLLGIITKKDVLKHIAQMANQDF
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258 AATGGAGGCAGCATTAACAGTTCTACACATTTACTGGATCTTTTGGATGAACCAATTCCA 317
                      AGCTATTATTTTCCTCTCAAAACTTTATGGAGATCATTTTTTGCTGCTTTAGTGGCTGCA
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AGCTACTATTTTCCCCTCAAAACATTGTGGCGTTCATTCTTTGCTGCCTTGGTGGCAGCA
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                                                                                                                                                                                           AACAAATACAGGAAGAATGAAGCCAAGCGCAGAGAGTCTTGTCGGCTGCAGCAGCAGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ninomiya,K., Wagatsuma,M., Kanda,K., Kondo,H., Yokoi,T., Kodaira,H., Furuya,T., Takahashi,M., Kikkawa,E., Omura,Y., Al Kodaira,H., Furuya,T., Takahashi,M., Kikkawa,E., Omura,Y., Al Kamihara,K., Katsuta,N., Sato,K., Tanikawa,M., Yamazaki,M., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishi: Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Murakawa,K., Kanehori,K., Takahashi-Fujii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
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Isogai,T., Otsuki,T.
Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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                                                              /Cell_type="teratocarcinoma"
/Clone_lib="NT2R97"
/note="cloning vector: pME18SFL3-mRNA from NT2 neuronal
precursor cells after 5-weeks retinoic acid (RA)
                                             induction
                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
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	CAACAGCAAAAAGAAAGAATCAGCATGGGAAATGACAAAA 437 	Y 378 AGAGAAAGGCATAGACGGATC 	Фр
	ATTTCCATACTATTGATTGGGTGCGAGAAAAATGTAAAGAC 377 	318 GGTGTTGGTACATATGATO	Qy Db
	TTCTACACATTTACTGGATCTTTTGGATGAACCAATTCCA 317 	258 AATGGAGGCAGCATTAAG 510 AATGGTGGAGGAATAGGT	Qy Db
· , . .	<pre>%; Score 1187; DB 9; Length 3046; %; Pred. No. 1.7e-200; 0; Mismatches 670; Indels 3; Gaps</pre>	Query Match Best Local Similarity 70.49 Matches 1602; Conservative	

2358	Qy	
2298 CTTCCAGCAGAAAGTCCTCGGGCCATTGAAGCTTCGAAGCATTCTTGACATGAGCCCTTTT	. Qy	
2238 AAAAAACAAGAAGGTATCGTTGGCAGTTCTCGGGTGTGTTTTGCACAGCACACCCCATCT	Оу	
2178	Оу	
2118 GAAAACATGATTAATGAAACCAGCTACAATGGATTTCCTGTCATAATGTCAAAAGAATCT	Qy Db	
2307 CGGAGAAATGATCCTTTGTTGACTGTCCTTACTCAGGACAGTATGACTGTGGAAGATGTA	da	
1998 2247	Db Oy	
N 14	Оу	
1878 ACTGGAGGCTTGGAATATATTGTTCCCCTTATGGCTGCAGTCATGACCAGTAAATGGGTT 	Фр	
1818 GCATGCTTAGGTGGTGACAAGAATGACTGTCTCCCTGGTGGTGATTGTTTTTGAGCTT	Оу	
7 1758 TGGTGTGAGGTCGGGGCTGATTGCATTACACCTGGCCTTTATGCCATGGTTGGT	Qy	
7 1698 GTGGGGATTGCGGTĞGAGCAGCTTGCCTACTATCACCACGACTGGTTTATCTTTAAGGAG	Qу	
7 1638 AAGGTTCCATCAGGCTTGTTCATCCCCAGCATGGCCATTGGAGCGATCGCAGGAAGGA	Оу	
7 1578 TGGCAGTTATGCCTGGCACTCATATTTAAAATCATAATGACAGTATTCACTTTTGGCATC	Qy Db	
7 1518 AGTAAAATTGTCGATGACATTCCTGATCGTCCAGCAGGCATTGGAGTATATTCAGCTATA 	Qy	
1458 ACAGACTGTGGTCCCCTGGAATCCTCTTCTCTTTGTGACTACAGAAATGACATGAATGCC	Qy Db	
/ 1398 ATAGCCTTCCCTAATCCATACACTAGGCTAAACACCAGTGAACTGATCAAAGAGCTTTTT	Qy	
/ 1338 ACGAAATTTGGAAAGTATCCCGTTCTGGAAGTCATTATTGTTGCAGCCATTACTGCTGTG	Оу	
/ 1278 GGGCTTTGGGGAGCCTTTTTCATTAGGGCAAATATTGCCTGGTGTCGTCGACGCAAGTCC	Оу	

